

WORTACH

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 16, 2000, 02:39:03 ; Search time 2352.22 Seconds
(without alignments)
-2062.792 Million cell updates/sec

Title: US-09-259-389-1
Perfect score: 1598
Sequence: 1 atggaacagacgtattga.....taggcgtttgcattccaagg 1598

Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

tabase: GenEmbl:*

Word size: 0

Number of hits that pass the threshold : 1642386

- 1: gb_ba1:*
- 2: gb_ba2:*
- 3: gb_ov:*
- 4: gb_ov:*
- 5: gb_pat:*
- 6: gb_ph:*
- 7: gb_pl1:*
- 8: gb_pl2:*
- 9: gb_pr1:*
- 10: gb_pr2:*
- 11: gb_pr3:*
- 12: gb_ro:*
- 13: gb_sts:*
- 14: gb_sy:*
- 15: gb_un:*
- 16: gb_v1:*
- 17: em_fun:*
- 18: em_hum1:*
- 19: em_hum2:*
- 20: em_in:*
- 21: em_om:*
- 22: em_or:*
- 23: em_ov:*
- 24: em_pat:*
- 25: em_ph:*
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- 27: em_ro:*
- 28: em_sts:*
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- 31: em_v1:*
- 32: gb_htg1:*
- 33: gb_htg2:*
- 34: gb_in1:*
- 35: gb_in2:*
- 36: gb_ba1:*
- 37: em_ba2:*
- 38: em_hum3:*
- 39: em_hum4:*
- 40: gb_pr4:*
- 41: gb_htg3:*
- 42: gb_htg4:*
- 43: gb_htg5:*
- 44: gb_htg6:*
- 45: gb_htg7:*
- 46: em_htg1:*
- 47: em_htg2:*
- 48: em_htg3:*
- 49: em_hum5:*

50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	1578.8	98.8	1847	12	AF044257	AF044257 Mus muscu	
2	1479.6	92.6	2490	40	AF130863	AF130863 Homo sapi	
3	557.2	34.9	986	4	AF024439	AF024439 Xenopus l	
4	404.2	25.3	1788	10	S80876	S80876 IKAROS-hik1	
5	398	24.9	1386	5	AR049700	AR049700 Sequence	
6	395.8	24.8	1557	4	GGIKTRF	Y11833 G.gallus mR	
7	392	24.5	3629	11	HS040462	U04062 Human Ikaro	
8	376	23.5	2688	12	AB017615	AB017615 Mus muscu	
9	364	22.8	2049	5	AR049702	AR049702 Sequence	
10	336	21.0	2496	4	OMU92201	U92201 Oncorhynch	
11	325	20.3	1521	12	AF001293	AF001293 Mus muscu	
12	316.8	19.8	2098	40	AF129512	AF129512 Homo sapi	
13	293.6	18.4	1485	4	GGA005933	AJ005933 Gallus ga	
14	286.6	17.9	1550	12	MUSIKAROS	L03547 Mouse Ikaro	
15	285.4	17.9	3923	4	AF186359	AF186359 Ambystoma	
16	285	17.8	1788	5	AR049699	AR049699 Sequence	
17	272.2	17.0	2183	4	OMU92200	U92200 Oncorhynch	
18	239.8	15.0	2301	4	OMU92198	U92198 Oncorhynch	
19	235.6	14.7	2309	4	AF092175	AF092175 Danio rer	
20	221.6	13.9	684	12	S74708	S74708 Ikaro/Lyf-	
21	192.8	12.1	1004	5	AR049705	AR049705 Sequence	
22	190.2	11.9	1296	5	AR049701	AR049701 Sequence	
23	177.6	11.1	2079	4	OMU92199	U92199 Oncorhynch	
24	174.4	10.9	415	4	XLU92202	U92202 Xenopus lae	
c	25	156.6	9.8	126836	44	AC013736	AC013736 Homo sapi
26	153.2	9.6	1170	5	AR049703	AR049703 Sequence	
27	146.6	9.2	1128	5	AR049704	AR049704 Sequence	
28	105.2	6.6	148640	4	AF056116	AF056116 Fugu rubr	
29	102.6	6.4	41081	41	AC010286	AC010286 Homo sapi	
c	30	102.6	6.4	80397	41	AC011502	AC011502 Homo sapi
c	31	102.6	6.4	90908	42	AC008463	AC008463 Homo sapi
32	100.8	6.3	118767	9	HS4PTEL	Z95704 Human DNA s	
33	100.8	6.3	2088	9	HS4PZNF1	Z96138 H.sapiens t	
34	100	6.3	3839	9	HUMRUPZN	L11672 Human Krupp	
35	97.8	6.1	2582	9	HUMZIFI	L32163 Homo sapien	
36	97.8	6.1	4208	11	AF011573	AF011573 Homo sapi	
37	97.8	6.1	2582	13	G28565	G28565 human STS S	
38	97.8	6.1	40404	41	AC011538	AC011538 Homo sapi	
39	97	6.1	236008	42	AC012616	AC012616 Homo sapi	
40	96.2	6.0	3003	10	HSZNF43	X59244 Human ZNF43	
41	94.6	5.9	2873	9	HUMHPLK	M55422 Human Kruep	
42	94.6	5.9	2873	13	G28705	G28705 SWS3976 Er	
43	94.6	5.9	2873	13	HUMSWS1269	GI2881 human chrom	
44	94.4	5.9	2985	11	HUMZNF1G	LI5309 Human zinc	
45	93.8	5.9	1434	12	MMNZFP	X52533 Mouse mRNA	

ALIGNMENTS

RESULT	1				
AF044257	AF044257	1847 bp	mRNA	ROD	04-FEB-1998
LOCUS	Mus musculus multi-zinc finger protein helios mRNA, complete cds.				
DEFINITION	AF044257				
ACCESSION	AF044257				
VERSION	AF044257.1	GI:2829276			
KEYWORDS					
SOURCE	house mouse.				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 1847)				

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* OM nucleic - nucleic search, using sw model

Run on: March 16, 2000, 03:23:33 ; Search time 2352.22 Seconds
(without alignments)
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Title: US-09-259-389-3
Perfect score: 1520
Sequence: 1 atggaacacagcgtattga.....taggcgttgcatccaagg 1520

Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl.*

Word size : 0

Number of hits that pass the threshold : 1642386

- 1: gb_bai.*
- 2: gb_ba2.*
- 3: gb_om.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_p11.*
- 8: gb_p12.*
- 9: gb_p13.*
- 10: gb_p14.*
- 11: gb_p15.*
- 12: gb_p16.*
- 13: gb_p17.*
- 14: gb_p18.*
- 15: gb_p19.*
- 16: gb_p20.*
- 17: gb_p21.*
- 18: gb_p22.*
- 19: gb_p23.*
- 20: gb_p24.*
- 21: gb_p25.*
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- 24: gb_p28.*
- 25: gb_p29.*
- 26: gb_p30.*
- 27: gb_p31.*
- 28: gb_p32.*
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- 30: gb_p34.*
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- 32: gb_p36.*
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- 36: gb_p40.*
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- 38: gb_p42.*
- 39: gb_p43.*
- 40: gb_p44.*
- 41: gb_p45.*
- 42: gb_p46.*
- 43: gb_p47.*
- 44: gb_p48.*
- 45: gb_p49.*
- 46: gb_p50.*
- 47: gb_p51.*
- 48: gb_p52.*
- 49: gb_p53.*

50: gb_p13.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	317.4	20.9	3629	11	HSU40462	U40462 Human Ikaro
8	289.6	19.1	1521	12	AF001293	AF001293 Mus muscu
9	286.4	18.8	2049	5	AR049702	AR049702 Sequence
10	285.8	18.8	1550	12	MUSIKAROS	L03547 Mouse Ikaro
11	285.4	18.8	3923	4	AF186359	AF186359 Ambystoma
12	284.2	18.7	1788	5	AR049699	AR049699 Sequence
13	283	18.6	2688	12	AB017615	AB017615 Mus muscu
14	279.2	18.4	2098	40	AF129512	AF129512 Homo sapi
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16	272.2	17.9	2183	4	OMU92201	U92201 Oncorhynch
17	247	16.2	1485	4	GGK005933	AJ005933 Gallus ga
18	216.4	14.2	2309	4	AF092175	AF092175 Daulio ier
19	192.8	12.7	1004	5	AR049705	AR049705 Sequence
20	179	11.8	2301	4	OMU92198	U92198 Oncorhynch
21	177.6	11.7	2079	4	OMU92199	U92199 Oncorhynch
22	174.4	11.5	415	4	XLU92202	U92202 Xenopus lae
23	164	10.8	684	12	S74708	S74708 IKAROS/LyF-
24	157.4	10.4	126836	44	AC013736	AC013736 Homo sapi
25	153.2	10.1	1170	5	AR049703	AR049703 Sequence
26	146.6	9.6	1296	5	AR049701	AR049701 Sequence
27	146.6	9.6	1128	5	AR049704	AR049704 Sequence
28	105.2	6.9	148640	4	AF056116	AF056116 Fugu rubr
29	81.4	5.4	1940	12	RNU67082	U67082 Rattus norv
30	81.2	5.3	3068	12	AF111101	AF111101 Mus muscu
31	80.2	5.3	236008	42	AC012616	AC012616 Homo sapi
32	80	5.3	1434	12	MMNZFP	X52533 Mouse mRNA
33	80	5.3	3492	12	MMZFP37F1	X89264 M.musculus
34	80	5.3	1949	11	MMZFP8	X64413 M.musculus
35	78.4	5.2	153875	11	AC003682	AC003682 Homo sapi
36	77.4	5.1	3839	9	HUMKRP2N	L11672 Human Krupp
37	76.6	5.0	118767	9	HS4PTEL	Z95704 Human DNA s
38	76.6	5.0	2088	9	HS4PZNF1	Z96138 H.sapiens t
39	75.8	5.0	147193	42	AC010467	AC010467 Homo sapi
40	75.4	5.0	1661	12	MMZ224763	AJ224763 Mus muscu
41	75.2	4.9	2971	12	AF072439	AF072439 Rattus no
42	75.2	4.9	206121	44	AC016769	AC016769 Homo sapi
43	75	4.9	2582	9	HUMZIFI	L32163 Homo sapien
44	75	4.9	3003	10	HSZNF43	X59244 Human ZNF43
45	75	4.9	4208	11	AF011573	AF011573 Homo sapi

ALIGNMENTS

RESULT	1	AF044257	1847 bp	mRNA	ROD	04-FEB-1998
AF044257		AF044257	1847 bp	mRNA	ROD	04-FEB-1998
LOCUS		Mus musculus multi-zinc finger protein helios mRNA, complete cds.				
DEFINITION		AF044257				
ACCESSION		AF044257.1				
VERSION		AF044257.1				
KEYWORDS		house mouse.				
SOURCE		Mus musculus				
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
		Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE		1 (bases 1 to 1847)				

AUTHORS Hahn, K., Cobb, B. S., McCarty, A. S., Brown, K. E., Klug, C. A., Lee, R.,
Akashi, K., Weismann, I. L., Fisher, A. G. and Smale, S. T.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-1998) HHMI/MSI, UCLA, 675 Circle Drive South, Box
951662, Los Angeles, CA 90095-1662, USA
FEATURES
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/db_xref="taxon:10090"

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/protein_id="AAC00513.1"
/db_xref="GI:282927"

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PLMHAPSTIAEVAFVSISSAYQVHPNRIERPISRETSDSHENMDGPTSLRPSR
PQREASPNSCLDSTSDSHDDRSYQGNPALNPKRKQSPAYMKEDVRLDAPKAP
KGSLLKDIYKVFNGEQEIQRAFKCEHCRVLFDRVMTYTHMGCHGYRDPLECNICGRS
ODRVFSSHIVRGHTPH"

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/note="encodes N-terminal zinc finger domain"

misc_feature 1594..1746
/note="encodes C-terminal zinc finger
domain/hunchback-like zinc fingers"

BASE COUNT 534 a 466 c 445 g 402 t

Query Match 92.9%; Score 1412.8; DB 12; Length 1847;
Best Local Similarity 94.4%; Fred. No. 0;
Matches 1508; Conservative 0; Mismatches 12; Indels 78; Gaps 1;

QY 1 atggaacacagcgtattggtggtatataacatgtgacatgagctttcacccgaagg 60
DB 178 ATGGAACACAGCGCAATTGATGCTATATAACATGTGACATGAGCTTTACCCGAAGG 237
QY 61 gaacacgcaatgcccattgacctcaccctcaagcagcccaatgagacacgtctcg 120
DB 238 GAACAGCGCAATATGCGCATTTGACCTTCACTCAGACACACCCATGAGACGCCCTCG 297
121 ccaagtccatgacagcaacaaattctgtaagctggaatgcaagtcagagtgatgaagtg 180
298 CCAAGTCACATGACAAAGCAAAATCTGTAAAGCTGGAATGCAAGTATGATGAAGAGTGT 357
QY 181 gacaggcagccctgagccgtgagatgagatcagagcagcccaatgagagcagccta 240
DB 358 GACAGGACGCCCTTGAGCGTGAGGATGAGATCAGGGGCCACCATGAGGGAGCGCCCTA 417
QY 241 gaagaaccccttaattgagagcgcgagtggtgcccacacaggaagtccagagaccttcaa 300
DB 418 GAAGAACCCTTAATTGAGAGCAGCGAGGTGGCCGACACAGGAAGTCCAGGACCTTCAA 477
QY 301 ggcgagggaggaatccggtctccgaa----- 327
DB 478 GCGGAGGGAGGATCCGGCTTCGGAATGGTAACTGAATGTACGCTCTGTGGCATGGTT 537
QY 327 -----tggtgagcgccttc 342
DB 538 TGCATTGGGGCCCAATGTGCTTATGTGTACATAAAGAGAGTCACATGTTGAGCGGCCCTC 597
QY 343 cactgtacacagtcgagagctctctttaccagagggcagacctctcgagacacataaag 402
DB 598 CACTGTAAACAGTGGGAGCTCTTTTACCCAGAGGGCAACCTTCTTGAGACACATAAAG 657
QY 403 ttacactctggagagagcccttcaaatgtccttctctgtatgctatctgttagaagagg 462
DB 658 TTACACTCTGGAGAGAAGCCCTTCAAAATGCTCTTCTGTAGCTATGCTTTGTAGAAGAG 717

QY 463 gacgctctcaacaggacacctcaactgagaccattctgtggttaaacctcaactgttaactac 522
DB 718 GAGCGCTCTCACAGGACACCTCAGAGCCCATTTCTGTGGTAAACCTCAAGTGTAACTAC 777
QY 523 tgtggccgaagctcaacagcagcgcagtcacgtcactggaggaacacacaggaagcgtgtcacac 582
DB 778 TGTGGCCGAAGCTACAAGCAGCGCAGCTCACTGGAGGAACACACAGGAACGCTGTACAC 837
QY 583 tatctcagaatgtcagcatggagggtgcgpggcaggttcattgagtcaccatgtacgcgct 642
DB 838 TATCTCCAAGTGTGAGTGGAGGTGCGGGCAGGTCATGAGTCACCATGTACCGCCT 897
QY 643 atggaagattgttaaggaacaagagcctatctatgggacaacaattctctgtggtgccttt 702
DB 898 ATGGAAGATTGTAGGAACAAGAGCCTATCATATGGACACATATTTCTCTGGTGCCTTT 957
QY 703 gagagacctgtctgtagagaagctcagcggaatattgggaagcgcaaaagctccact 762
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QY 763 cctcagaagttgtgggggaaaagccttatgagctcagctaccagatatcttattgat 822
DB 1018 CCTCAGAAGTTGTGGGGGAAAAGCTTATGCGATTTCAGCTACCCAGATATTCATTTGAT 1077
QY 823 atgaacttaacatatgagaagggtgcgagctgagctgagctcagcttattctcaggtctatcat 882
DB 1078 ATGAACCTTAACATATGAGAAGGAGGCTGAGCTGATGTCAGTCTCATATGATGGACCAAGCC 1137
QY 883 atcaacaatgaaatcactcactctgagctgagctgagggccttcacccctctgagtcgagcatgca 942
DB 1138 ATCAACAATGCAATCACTACCTTTGAGCTGAGGCGCTTACCCTCTGATGTCAGCATGCA 1197
QY 943 caagcacaactcgtcgtgaggtggcccgagttataagctcagcttattctcaggtctatcat 1002
DB 1198 CCAAGCAAAATCGTGTAGGTGGCCCGCCAGTTATAAGCTCAGCTTATTTCTCAGGTCTATCAT 1257
QY 1003 ccaacagagtagaagaagcatttagcagggaaacatctgtagtcacgaaaaacaacatg 1062
DB 1258 CCAAACAGGATAGAAGACCCATTAGCAGGGAACATCTGATATGTCACGAAAAACAACATG 1317
QY 1063 gatggcccatctctcattcagacacaaagagtcagccccaggaagagagagcgtcgcgc 1122
DB 1318 GATGGCCCATCTTCTCATACACCAAGAGTGCACCCAGGAAGAGAGGCGCTCGCCC 1377
QY 1123 agcaatagctcctcgtattctactgactcagaaagtagccatgagccagccagctcctac 1182
DB 1378 AGCAATAGTGTGCTCGATTCTACTGACTCAGAAAGTAGCCATGATGACCCAGTCTTAC 1437
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DB 1438 CAAGGAACCCGTGCTTAAATCCAAAGAGGAACAAAGCCAGCTTACATGAAGAGGAGAT 1497
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DB 1498 GTCAAGGCTTTGGATGTACTCAAGAGCCCCCAAGGGCTCTCTGAAAGGACATCTATAAGTT 1557
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DB 1558 TTCATGTGAGAGAGAGAACAGATPAAGGGCTTCAAGTGTGAGCACTGCCAGTCTCTTTT 1617
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QY 1483 gggcagacacattccactaggcggtttgattcccaag 1520
DB 1738 GGGGAGCACACATTCCTACCTAGGCGCTTTTCATTCCTCAAG 1775

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 16, 2000, 03:24:16 ; Search time 2352.22 Seconds
(without alignments)
-2487.485 Million cell updates/sec

Title: US-09-259-389-5
Perfect score: 1927
Sequence: 1 gccgggcagctgcattgc.....gcagtgctattgctgtctgt 1927

Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

abase : GenEmbl:*

Word size : 0

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- 8: gb_p12.*
- 9: gb_p11.*
- 10: gb_p11.*
- 11: gb_p11.*
- 12: gb_p11.*
- 13: gb_p11.*
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- 16: gb_p11.*
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- 19: em_fun.*
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- 22: em_in.*
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- 45: gb_htg7.*
- 46: gb_htg7.*
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12	331.2	17.2	2098	40	AF129512	Homo sapi
13	298.4	15.5	1485	4	GGA005933	Gallus ga
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ALIGNMENTS

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DEFINITION	Homo sapiens	zinc finger DNA binding protein Helios mRNA, complete cds.				
ACCESSION	AF130863					
VERSION	AF130863.1	GI:6457257				
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REFERENCE 1 (bases 1 to 2490)
AUTHORS Hosokawa, Y., Maeda, Y. and Seto, M.
TITLE Human Helios, an Ikaros-related zinc finger DNA binding protein:
        DNA cloning and tissue expression pattern
JOURNAL Immunogenetics 50 (1-2), 106-108 (1999)
MEDLINE 20009537
REFERENCE 2 (bases 1 to 2490)
AUTHORS Hosokawa, Y., Maeda, Y. and Seto, M.
TITLE Direct Submission
JOURNAL Submitted (24-FEB-1999) Lab. of Chemotherapy, Aichi Cancer Center
        Research Institute, 1-1 Kanakoden, Chikusa-ku, Nagoya, Aichi
        464-8681, Japan
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DEFINITION Mus musculus multi-zinc finger protein helios mRNA, complete cds.
ACCESSION AF044257
VERSION AF044257.1 GI:2829276
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1847)
AUTHORS Hahn,K., Cobb,B.S., McCarty,A.S., Brown,K.F., Klug,C.A., Lee,R.,
Akashi,K., Weissmann,I.L., Fisher,A.G. and Smale,S.F.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-1998) HMI/M&I, UCLA, 675 Circle Drive South, Box
951662, Los Angeles, CA 90095-1662, USA
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REFERENCE	1 (bases 1 to 986)		
AUTHORS	Turpen,J., Kelley,C., Mead,P. and Zon,L.		
TITLE	Bi-Potential Primitive-Definitive Hematopoietic Progenitors in the Vertebrate Embryo		
JOURNAL	Immunity (1997) In press		
REFERENCE	2 (bases 1 to 986)		
AUTHORS	Turpen,J., Kelley,C., Mead,P. and Zon,L.		
TITLE	Direct Submision		
JOURNAL	Submitted (10-SEP-1997) Hematology, Children's Hospital, 300 Longwood Ave, Boston, MA 02115, USA		
FEATURES	Location/Qualifiers		

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QY	978	tctctcatagagaagctcagggggaatatggaaaaacgtataaagctccactcaaaaa	1037
Db	308	GGCTGTTATAGAGACTTTCAGCAGCAACATGGGGAAGGTAAAGAGTCCACCCACAGAG	367
QY	1038	gttttggggaaagctcgtcgattcgcagctaccagatattcactttgatgatgaactt	1097
Db	368	GTTTTGGGTGAGAAGCTCATGAGATATGGATATCTCTGACTTGCACCTTTGATATG----	423
QY	1098	aaatatgagaagagagcgtgagctgagctcagctcctcatatgatggacacacacaa	1157
Db	423	-GCCATAGAAAAGAGCAGAAATAATCCAGTCACAAATGATGGATCAGCGGATTAACAA	481
QY	1158	tgcaatcacctaccttgagcgtgagcccttcaacctctgagcagccccccaagc	1217
Db	482	TGCTATAACATACCTGGGAGCAGTCACTGGGGCTCTCATACACCATCAGCAGCTGC	541
QY	1218	aatcgcgtgaagtggcccgcttataagctcagcttattctcaggtctatcatccaaatag	1277
Db	542	CATGCTGAGGTTCCACCAATTTCTAGTTTCACTTTACTCTCAGGTCTATCATCCGCCAG	601
QY	1278	gataagaagaccatttgagggaactgctgatgatgataaacaacatgagatggccc	1337
Db	602	AGTGGAGAGACCCACAGGAGGAGACATCAGACGACACGATAAACAATGGATGGGCC	661
QY	1338	catctctctcatcagacaaagagtcgacccaggaagagagcctctccagcagcag	1397
Db	662	AATCTCCCTTATCAGAACAAAGAACCCCTTCAGGAGAGGAGGCATCACCACCAACAG	721
QY	1398	ctgctgtgattccactgactcagaaagcagcgaatgatgacccagctccttaccagagaca	1457
Db	722	CTGCTTTGATATACTACTGACTCAGAAAGAGCCATGAGGCACCGCAATCTCTACCGGCAA	781